SEQUENCE LISTING

<110> GIMENO, Ruth

<120> METHODS FOR THE TREATMENT OF METABOLIC
      DISORDERS, INCLUDING OBESITY AND DIABETES

<130> MNI-220

<150> 60/271,655
<151> 2001-02-26

<160> 16

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (44)...(1129)

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tgc gcg cgg gca gcg ggc gac gcg ccc ttg cgc agc ctg gag caa gcc   103
Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser Leu Glu Gln Ala
 5   10   15   20

aac cgc acc cgc ttt ccc ttc ttc tcc gac gtc aag ggc gac cac cgg   151
Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys Gly Asp His Arg
                25   30   35

ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt gca   199
Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe Ala
            40   45   50

gtg tcg ctg ctg ggc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc cga   247
Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg Arg
        55   60   65

cga cgc cgc ggc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc gcg   295
Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys Ala
    70   75   80

gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc tgg   343
Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg Trp
 85   90   95   100

act gag gcc tgg ctg ctg ggc ccc gtt gcc tgc cac ctg ctc ttc tac   391
Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe Tyr
                105   110   115

gtg atg acc ctg agc ggc agc gtc acc atc ctc acg ctg gcc gcg gtc   439
Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala Val

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                 120                      125                      130

agc ctg gag cgc atg gtg tgc atc gtg cac ctg cag cgc ggc gtg cgg    487
Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val Arg
        135                 140                 145

ggt cct ggg cgg cgg gcg cgg gca gtg ctg ctg gcg ctc atc tgg ggc    535
Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp Gly
        150                 155                 160

tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttt cga gtc gtc    583
Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val Val
165                 170                 175                 180

ccg caa cgg ctc ccc ggc gcc gac cag gaa att tcg att tgc aca ctg    631
Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser Ile Cys Thr Leu
                185                 190                 195

att tgg ccc acc att cct gga gag atc tcg tgg gat gtc tct ttt gtt    679
Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp Val Ser Phe Val
                200                 205                 210

act ttg aac ttc ttg gtg cca gga ctg gtc att gtg atc agt tac tcc    727
Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val Ile Ser Tyr Ser
                215                 220                 225

aaa att tta cag atc aca aag gca tca agg aag agg ctc acg gta agc    775
Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg Leu Thr Val Ser
        230                 235                 240

ctg gcc tac tcg gag agc cac cag atc cgc gtg tcc cag cag gac ttc    823
Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser Gln Gln Asp Phe
245                 250                 255                 260

cgg ctc ttc cgc acc ctc ttc ctc ctc atg gtc tcc ttc ttc atc atg    871
Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser Phe Phe Ile Met
                265                 270                 275

tgg agc ccc atc atc atc acc atc ctc ctc atc ctg atc cag aac ttc    919
Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu Ile Gln Asn Phe
                280                 285                 290

aag caa gac ctg gtc atc tgg ccg tcc ctc ttc ttc tgg gtg gtg gcc    967
Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe Trp Val Val Ala
        295                 300                 305

ttc aca ttt gct aat tca gcc cta aac ccc atc ctc tac aac atg aca   1015
Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Asn Met Thr
        310                 315                 320

ctg tgc agg aat gag tgg aag aaa att ttt tgc tgc ttc tgg ttc cca   1063
Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys Phe Trp Phe Pro
325                 330                 335                 340

gaa aag gga gcc att tta aca gac aca tct gtc aaa aga aat gac ttg   1111
Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys Arg Asn Asp Leu
                345                 350                 355

tcg att att tct ggc taa tttttcttta tagccgagtt tctcacacct         1159
Ser Ile Ile Ser Gly  *
                360
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ggcgagctgt ggcatgcttt taaacagagt tcatttccag taccctccat cagtgcaccc 1219
tgctttaaga aaatgaacct atgcaaatag acatccacag cgtcggtaaa ttaaggggtg 1279
atcaccaagt ttcataatat tttcccttta taaaaggatt tgttggccag gtgcagtggt 1339
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gttcgagacc aacctgacca acatggtgag accccccgtct ctactaaaaa taaaaaaaaa 1459
aattagctgg gagtggtggt gggcacctgt aatcctagct acttgggagg ctgaaccagg 1519
agaatctctt gaacctggga ggcagaggtt gcagtgagcc gagatcgtgc cattgcactc 1579
caaccagggc aacaagagtg aaactccatc ttaaaaaaaa aaaaaaaaag atttgttatg 1639
ggttcctttt aaatgtgaac ttttttagtg tgtttgtaat atgatcaaat ttaataaata 1699
tttatttatg actgttcagc aaaaaaaaaa aaaaaaaagg gcgg                 1743
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<210> 2
<211> 361
<212> PRT
<213> Homo sapiens
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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
                20                  25                  30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
            35                  40                  45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
        50                  55                  60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65                  70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
                85                  90                  95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
        115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
        130                 135                 140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145                 150                 155                 160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
            180                 185                 190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
        195                 200                 205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
        210                 215                 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225                 230                 235                 240
Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
                245                 250                 255
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
            260                 265                 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
        275                 280                 285
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
        290                 295                 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                 310                 315                 320
Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
                325                 330                 335
Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
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          340                     345                    350
Arg Asn Asp Leu Ser Ile Ile Ser Gly
        355                 360


<210> 3
<211> 1086
<212> DNA
<213> Homo sapiens

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gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc 180
gccctggtgc tggtggcgcg ccgacgacgc gcggcgcga ctgcctgcct ggtactcaac 240
ctcttctgcg cggacctgct cttcatcagc gctatccctc tggtgctggc cgtgcgctgg 300
actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgaccctg 360
agcggcagcg tcaccatcct cacgctggcc gcggtcagcc tggagcgcat ggtgtgcatc 420
gtgcacctgc agcgcggcgt gcggggtcct gggcggcggg cgcgggcagt gctgctggcg 480
ctcatctggg gctattcggc ggtcgccgct ctgcctctct gcgtcttctt cgagtcgtc 540
ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc 600
attcctggag agatctcgtg ggatgtctct tttgttactt tgaacttctt ggtgccagga 660
ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg 720
ctcacggtaa gcctggccta ctcggagagc caccagatcc gcgtgtccca gcaggacttc 780
cggctcttcc gcaccctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc 840
atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg 900
tccctcttct ctgggtggt ggccttcaca tttgctaatt cagccctaaa ccccatcctc 960
tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
gaaaagggag ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
ggctaa                                                           1086


<210> 4
<211> 1560
<212> DNA
<213> Murine ortholog

<220>
<221> CDS
<222> (195)...(1280)


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ttcacaccat cagtgaccac tccagacttg tccggcttta cccgaatctt cacagcggag 120
tcgatgaccc tcttgacagc cacgagcgcg cgcagctccg ccatcttccc ggacgcgtgg 180
gccgggcgcc cggc atg tcc cct gag tgt gca cag acg acg ggc cct ggt 230
                 Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly
                  1               5                   10

ccc tcg cac acc ctg gac caa gtc aat cgc acc cac ttc cct ttc ttc 278
Pro Ser His Thr Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe
            15                  20                  25

tcg gat gtc aag ggc gac cac cgg ttg gtg ttg agc gtc gtg gag acc 326
Ser Asp Val Lys Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr
    30                  35                  40

acc gtt ctg gga ctc atc ttt gtc gtc tca ctg ctg ggc aac gtg tgt 374
Thr Val Leu Gly Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys
45                  50                  55                  60

gct cta gtg ctg gtg gcg cgc cgt cgg cgc cgt ggg gcg tca gcc agc 422
```

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Ala Leu Val Leu Val Ala Arg Arg Arg Arg Arg Gly Ala Ser Ala Ser
            65                    70                75


ctg gtg ctc aac ctc ttc tgc gcg gat ttg ctc ttc acc agc gcc atc    470
Leu Val Leu Asn Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile
            80                    85                90


cct cta gtg ctc gtc gtg cgc tgg act gag gcc tgg ctg ttg ggg ccc    518
Pro Leu Val Leu Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro
            95                    100               105


gtc gtc tgc cac ctg ctc ttc tac gtg atg aca atg agc ggc agc gtc    566
Val Val Cys His Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val
    110                   115               120


acg atc ctc aca ctg gcc gcg gtc agc ctg gag cgc atg gtg tgc atc    614
Thr Ile Leu Thr Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile
125               130               135                   140


gtg cgc ctc cgg cgc ggc ttg agc ggc ccg ggg cgg cgg act cag gcg    662
Val Arg Leu Arg Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala
            145               150               155


gca ctg ctg gct ttc ata tgg ggt tac tcg gcg ctc gcc gcg ctg ccc    710
Ala Leu Leu Ala Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro
            160               165               170


ctc tac atc ttg ttc cgc gtg gtc ccg cag cgc ctt ccc ggc ggg gac    758
Leu Tyr Ile Leu Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp
        175               180               185


cag gaa att ccg att tgc aca ttg gat tgg ccc aac cgc ata gga gaa    806
Gln Glu Ile Pro Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu
    190               195               200


atc tca tgg gat gtg ttt ttt gag act ttg aac ttc ctg gtg ccg gga    854
Ile Ser Trp Asp Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly
205               210               215               220


ctg gtc att gtg atc agt tac tcc aaa att tta cag atc acg aaa gca    902
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala
            225               230               235


tcg cgg aag agg ctt acg ctg agc ttg gca tac tct gag agc cac cag    950
Ser Arg Lys Arg Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln
            240               245               250


atc cga gtg tcc caa caa gac tac cga ctc ttc cgc acg ctc ttc ctg    998
Ile Arg Val Ser Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu
            255               260               265


ctc atg gtt tcc ttc ttc atc atg tgg agt ccc atc atc atc acc atc   1046
Leu Met Val Ser Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile
    270               275               280


ctc ctc atc ttg atc caa aac ttc cgg cag gac ctg gtc atc tgg cca   1094
Leu Leu Ile Leu Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro
285               290               295               300


tcc ctt ttc ttc tgg gtg gtg gcc ttc acg ttt gcc aac tct gcc cta   1142
Ser Leu Phe Phe Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu
```

```
                    305                      310                        315

aac ccc ata ctg tac aac atg tcg ctg ttc agg aac gaa tgg agg aag   1190
Asn Pro Ile Leu Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys
            320                 325                 330

att ttt tgc tgc ttc ttt ttt cca gag aag gga gcc att ttt aca gat   1238
Ile Phe Cys Cys Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp
            335                 340                 345

acg tct gtc agg cga aat gac ttg tct gtt att tcc agc taa           1280
Thr Ser Val Arg Arg Asn Asp Leu Ser Val Ile Ser Ser  *
            350                 355                 360


ctagcctctg gtgccaggtg aaccacggtg tgcatgtaaa gggagttaac ttcaaggaaa 1340
gcccaccagt gcgccctgct ttaaaaatac ccgacttcca acagcaggca tctacggagc 1400
cagcaaatta aggaatgatc gctcagtata aaaatatttt tccttaaaag aactttctat 1460
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<210> 5
<211> 361
<212> PRT
<213> Murine ortholog

<400> 5
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1               5                   10                  15
Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
            20                  25                  30
Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
        35                  40                  45
Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
    50                  55                  60
Val Ala Arg Arg Arg Arg Gly Ala Ser Ala Ser Leu Val Leu Asn
65              70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
            85                  90                  95
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
            115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
            130                 135                 140
Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
145                 150                 155                 160
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Tyr Ile Leu
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
            180                 185                 190
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
            195                 200                 205
Val Phe Phe Glu Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
    210                 215                 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225                 230                 235                 240
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
                245                 250                 255
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
            260                 265                 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
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        275                    280                    285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
    290                    295                    300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                    310                    315                    320
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
                   325                    330                    335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
                   340                    345                    350
Arg Asn Asp Leu Ser Val Ile Ser Ser
                   355                    360
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<210> 6
<211> 1086
<212> DNA
<213> Murine ortholog

<400> 6
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gtcgtggaga ccaccgttct gggactcatc tttgtcgtct cactgctggg caacgtgtgt 180
gctctagtgc tggtggcgcg ccgtcggcgc cgtggggcgt cagccagcct ggtgctcaac 240
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actgaggcct ggctgttggg gcccgtcgtc tgccacctgc tcttctacgt gatgacaatg 360
agcggcagcg tcacgatcct cacactggcc gcggtcagcc tggagcgcat ggtgtgcatc 420
gtgcgcctcc ggcgcggctt gagcggcccg gggcggcgga ctcaggcggc actgctggct 480
ttcatatggg gttactcggc gctcgccgcg ctgcccctct acatcttgtt ccgcgtggtc 540
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cgcataggag aaatctcatg ggatgtgttt tttgagactt tgaacttcct ggtgccggga 660
ctggtcattg tgatcagtta ctccaaaatt ttacagatca cgaaagcatc gcggaagagg 720
cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac 780
cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc 840
atcatcacca tcctcctcat cttgatccaa aacttccggc aggacctggt catctggcca 900
tcccttttct tctgggtggt ggccttcacg tttgccaact ctgccctaaa ccccatactg 960
tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt ctttttttcca 1020
gagaagggag ccattttttac agatacgtct gtcaggcgaa atgacttgtc tgttatttcc 1080
agctaa                                                          1086
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<210> 7
<211> 20
<212> DNA
<213> Murine ortholog

<400> 7
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acttcaagga aagcccacca                                                20
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<210> 8
<211> 20
<212> DNA
<213> Murine ortholog

<400> 8
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tccgtagatg cctgctgttg                                                20
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<210> 9
<211> 27
<212> DNA
<213> Murine ortholog

<400> 9

tgcgccctgc tttaaaaata cccgact   27

<210> 10
<211> 19
<212> DNA
<213> Homo sapiens

<400> 10
acctgggagg cagaggttg   19

<210> 11
<211> 20
<212> DNA
<213> Homo sapiens

<400> 11
tcttgttgcc ctggttggag   20

<210> 12
<211> 24
<212> DNA
<213> Homo sapiens

<400> 12
agtgagccga gatcgtgcca ttgc   24

<210> 13
<211> 21
<212> DNA
<213> Homo sapiens

<400> 13
gcgccgggaa tgtcccctga a   21

<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<400> 14
ttgtcgatta tttctggcta a   21

<210> 15
<211> 18
<212> DNA
<213> Homo sapiens

<400> 15
ccgggcatgt cccctgag   18

<210> 16
<211> 18
<212> DNA
<213> Homo sapiens

<400> 16
tctgttattt ccagctaa   18